

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.  
Baker, Kevin  
Chuntharapai, Anan  
Gurney, Austin  
Kim, Kyung Jin  
10 Wood, William

(ii) TITLE OF INVENTION: Apo-2DcR

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

30 (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 12-Jun-1998  
(C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/049911

(B) FILING DATE: 18-JUN-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1110P1

(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: 650/225-5416

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val  
1 5 10 15

Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg  
20 25 30

Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg  
35 40 45

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His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser  
50 55 60

Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr  
65 70 75

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	Thr	Asn	Ala	Ser	Asn	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	
					80					85					90	
5	Cys	Lys	Ser	Asp	Gln	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	
					95					100					105	
	Asp	Thr	Val	Cys	Gln	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	
					110					115					120	
10	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	
					125					130					135	
	Val	Gln	Val	Ser	Asn	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	
					140					145					150	
	Glu	Glu	Phe	Gly	Ala	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	
					155					160					165	
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					170					175					180	
	Glu	Thr	Met	Asn	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					185					190					195	
25	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					200					205					210	
	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	
					215					220					225	
30	Glu	Thr	Met	Thr	Thr	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	
					230					235					240	
	Leu	Ser	Cys	Thr	Ile	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu	
35					245					250					255	

Ile Val Phe Val

259

(2) INFORMATION FOR SEQ ID NO:2:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1180 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100

CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150

AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195

Met

1

GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234

Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile

5

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GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273

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Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr

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ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312

Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala

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TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170

5 AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly  
-40 -35 -30

Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro  
-25 -20 -15

Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro  
-10 -5 1 5

Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro  
10 15 20

Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro  
25 30 35

Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly  
40 45 50

Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala  
55 60 65

03095000-091000

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn  
70 75 80

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln  
5 85 90 95

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln  
100 105 110

Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys  
10 115 120 125

Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn  
130 135 140

Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala  
145 150 155

Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr  
160 165 170

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr  
175 180 185

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr  
25 190 195 200

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr  
205 210 215

Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr  
30 220 225 230

Ser Pro Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile  
35 235 240 245



Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
250 255 259

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1180 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50

ATTTTGGGA GTTTGACCAG AG	ATG CAA GGG GTG AAG GAG 90
	Met Gln Gly Val Lys Glu
	-40 -35

CGC TTC CTA CCG TTA GGG AAC TCT GGG GAC AGA GCG CCC 129
Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
-30 -25

CGG CCG CCT GAT GGC CGA GGC AGG GTG CGA CCC AGG ACC 168
Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
-20 -15 -10

CAG GAC GGC GTC GGG AAC CAT ACC ATG GCC CGG ATC CCC 207
Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
-5 1 5

AAG ACC CTA AAG TTC GTC GTC GTC ATC GTC GCG GTC CTG 246
Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
10 15



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GTC CAA GTC AGT AAT TGT ACG TCC TGG GAT GAT ATC CAG 636  
Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln  
140 145

5 TGT GTT GAA GAA TTT GGT GCC AAT GCC ACT GTG GAA ACC 675  
Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr  
150 155 160

10 CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCG GGG ACT 714  
Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr  
165 170

CCT GCC CCA GCT GCT GAA GAG ACA ATG AAC ACC AGC CCA 753  
Pro Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro  
175 180 185

GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG ACC ACC 792  
Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Thr Thr  
190 195 200

AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG 831  
Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met  
205 210

ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG 870  
Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu  
215 220 225

30 ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC TCT TCT CAT 909  
Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His  
230 235

35 TAC CTC TCA TGC ACC ATC GTA GGG ATC ATA GTT CTA ATT 948  
Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile  
240 245 250

GTG CTT CTG ATT GTG TTT GTT T GAAAGACTTC ACTGTGGAAG 990  
Val Leu Leu Ile Val Phe Val  
255 259

5 AAATTCCTTC CTTACCTGAA AGGTTCAGGT AGGCGCTGGC TGAGGGCGGG 1040  
GGGCGCTGGA CACTCTCTGC CCTGCCTCCC TCTGCTGTGT TCCCACAGAC 1090  
AGAAACGCCT GCCCCTGCCC CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140  
10 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1180

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTAACACGA CGGCCAGTTA AATAGACCTG CAATTATTAA TCT 43

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAAACAG CTATGACCAC CTGCACACCT GCAAATCCAT T 41

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His  
1 5 10 15  
Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly  
20 25 30  
Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys  
35 40 45  
Gly Cys Arg Lys  
49

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn  
1 5 10 15

Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln  
20 25 30

Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln  
5 35 40 45

Cys Lys Glu  
48

10 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

5 CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145  
Met Glu  
1

10 CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184  
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
5 10 15

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223  
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala  
20 25

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262  
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val  
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301  
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala  
45 50

25 CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340  
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala  
55 60 65

30 GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379  
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu  
70 75 80

35 TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418  
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp  
85 90









GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTTGGTT TGGGATGTCA 1650

TTGTTTTTCAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

5 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:11:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg  
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro  
20 25 30

Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val  
35 40 45

Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp  
50 55 60

30 Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser  
65 70 75

Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp  
80 85 90

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Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro  
275 280 285

5 Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala  
290 295 300

Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp  
305 310 315

10 Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg  
320 325 330

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu  
335 340 345

Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp  
350 355 360

Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp  
365 370 375

Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu  
380 385 390

25 Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
395 400 405

Ala Asp Ser Ala Xaa Ser  
410 411

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

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(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:13:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30